

QY 361 PLASIDRLV-----NYDRLRVNYDRLRVNYDRLRV 392
 DB 359 PLATIDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 418
 QY 393 YDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 437
 DB 419 YDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 463

RESULT 2

025366 PRELIMINARY; PRT; 476 AA.
 ID 025366
 AC 025366
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Fucosyltransferase.
 GN OrderedLocustNames=HP0651;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteriaceae; Helicobacter.
 OX NCBI_TaxID=210;

SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
 RA Tomb J.-F., White O., Kervilange A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
 RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
 RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
 RA Glodek A., McMeany K., Fitzgerald L.M., Lee N., Adams M.D.,
 RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
 RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
 RA Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
 RA Smith H.O., Fraser C.M., Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori."
 RL Nature 388:539-547(1997).
 DR EMBL; AB000578; AAD07710.1; -
 DR PIR; C64601; C64601.
 DR TIGR; HP0651; -
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IBA.
 DR KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 476 AA; 55926 MW; 328FDBD36B1F74 CRC64;

Query Match 86.2%; Score 2058.5; DB 2; Length 476;
 Best Local Similarity 84.5%; Pred. No. 7.3e-130;
 Matches 394; Conservative 13; Mismatches 28; Indels 31; Gaps 3;

QY 1 MFQPLDLYVESASIEKMAKSKS-PPPLKIAVANMWDGDEIKKPKSVLYPIFSQRTIAL 59
 DB 1 MFQPLDLYVESASIEKMAKSKSPPPLKIAVANMWDGDEIKKPKSVLYPIFSQRTIAL 60
 QY 60 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGNEVPENFNLFDVAIGDELDPRDY 119
 DB 61 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGNEVPENFNLFDVAIGDELDPRDY 120
 QY 120 LRMPLYYRLHKKASVNDTTSPIYKQNSLYTLKKPSHQPKENPNLCVVNDSDPLK 179
 DB 121 LRMPLYYRLHKKASVNDTTSPIYKQNSLYTLKKPSHQPKENPNLCVVNDSDPLK 180
 QY 180 RGVSFVSNANNAFPRNAFYDALNSIEPVYGGGSKVNTLGYVNGKSEFLSQYKFNLCFE 239
 DB 181 RGVSFVSNANNAFPRNAFYDALNSIEPVYGGGSKVNTLGYVNGKSEFLSQYKFNLCFE 240
 QY 240 NSQGYGVTEKILDAVFSHTIPIYWGSPVAKDFNPKSEFVNVHDENNDAIDYIKYLAHT 299
 DB 241 NSQGYGVTEKILDAVFSHTIPIYWGSPVAKDFNPKSEFVNVHDENNDAIDYIKYLAHT 300
 QY 300 HPNAYLDMLYENPPLNTLDGKAYFYODLSFKKILAFPTILNDTIYHKSSTSPMWECDLD 359
 DB 301 HPNAYLDMLYENPPLNTLDGKAYFYODLSFKKILAFPTILNDTIYHKSSTSPMWECDLD 358

QY 360 EPLASI-----DRLRVNYDRLRVNYDRLRVNYDRLRV 391
 DB 359 EPLASIDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 418
 QY 392 NYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 437
 DB 419 NYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRVNYDRLRV 464

RESULT 3

025142 PRELIMINARY; PRT; 425 AA.
 ID 025142
 AC 025142
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Fucosyltransferase.
 GN OrderedLocustNames=HP0379;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteriaceae; Helicobacter.
 OX NCBI_TaxID=210;

SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
 RA Tomb J.-F., White O., Kervilange A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
 RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
 RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
 RA Glodek A., McMeany K., Fitzgerald L.M., Lee N., Adams M.D.,
 RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
 RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
 RA Wathey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
 RA Smith H.O., Fraser C.M., Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori."
 RL Nature 388:539-547(1997).
 DR EMBL; AB000554; AAD07447.1; -
 DR PIR; C64567; C64567.
 DR TIGR; HP0379; -
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IBA.
 DR KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 425 AA; 49329 MW; 1182AF180D124A34 CRC64;

Query Match 82.6%; Score 1972.5; DB 2; Length 425;
 Best Local Similarity 85.8%; Pred. No. 3.7e-124;
 Matches 376; Conservative 9; Mismatches 24; Indels 29; Gaps 2;

QY 1 MFQPLDLYVESASIEKMAKSKS-PPPLKIAVANMWDGDEIKKPKSVLYPIFSQRTIAL 59
 DB 1 MFQPLDLYVESASIEKMAKSKSPPPLKIAVANMWDGDEIKKPKSVLYPIFSQRTIAL 60
 QY 60 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGNEVPENFNLFDVAIGDELDPRDY 119
 DB 61 HONPNEFSDLVFNSPLGSAKILSYONAKRVYTGNEVPENFNLFDVAIGDELDPRDY 120
 QY 120 LRMPLYYRLHKKASVNDTTSPIYKQNSLYTLKKPSHQPKENPNLCVVNDSDPLK 179
 DB 121 LRMPLYYRLHKKASVNDTTSPIYKQNSLYTLKKPSHQPKENPNLCVVNDSDPLK 180
 QY 180 RGVSFVSNANNAFPRNAFYDALNSIEPVYGGGSKVNTLGYVNGKSEFLSQYKFNLCFE 239
 DB 181 RGVSFVSNANNAFPRNAFYDALNSIEPVYGGGSKVNTLGYVNGKSEFLSQYKFNLCFE 240
 QY 240 NSQGYGVTEKILDAVFSHTIPIYWGSPVAKDFNPKSEFVNVHDENNDAIDYIKYLAHT 299
 DB 241 NSQGYGVTEKILDAVFSHTIPIYWGSPVAKDFNPKSEFVNVHDENNDAIDYIKYLAHT 300
 QY 300 HPNAYLDMLYENPPLNTLDGKAYFYODLSFKKILAFPTILNDTIYHKSSTSPMWECDLD 359
 DB 301 HPNAYLDMLYENPPLNTLDGKAYFYODLSFKKILAFPTILNDTIYHKSSTSPMWECDLD 360

Oy		360	BPLASIDDDLRNVYDRLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNYDDLRVNNSAPLLE	419
Dd		361	KPLVSIDDDLNRVNYDDLRVNYD-----	RLONNSAPLLE 392
Oy		420	LSONTSPFKYRKAYOKPI 437	
Dd		393	LSONTTFKRYKAYOKSL 410	
 RESULT 4				
O9ZLI3				
ID	O9ZLI3	PRELIMINARY;	PRT:	454 AA.
AC	O9ZLI3;			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	ALPHA (1,3)-FUCOSYLTRANSFERASE.			
GN	Name=func1; OrderedLocusNames=JHNP0596;			
OS	Helicobacter pylori J99 (Campylobacter pylori J99).			
OC	Bacteria; Proteobacteria; Bpsilomproteobacteria; Campylobacterales;			
OC	Helicobacteraceae; Helicobacter.			
OX	NCBI_taxid=85963;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;			
RA	Alm R.A., Ling L.-S.L., Molt D.T., King B.L., Brown B.D., Dotz P.C.,			
RA	Smith D.R., Noonan A.B., Guild B.C., deJonge B.L., Carmel G.,			
RA	Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,			
RA	Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,			
RA	Trust T.J.;			
RT	"Genomic sequence comparison of two unrelated isolates of the human			
RT	gastric pathogen Helicobacter pylori.";			
RL	Nature 397:176-180(1999).			
DR	EMBL, AB001491, AAD06169.1; -			
DR	PIR, B71914; B71914.			
KM	GO, GO:0016757; P:transferase activity; Transferring glycosyl. . ; IRA.			
KM	Complete proteome; Glycosyltransferase; Transferase			
SQ	SEQUENCE 454 AA; 5348 MW; 3262687131263ABO CRC64;			

[illegible]

Db	917	ONASPILESONTFFCYKAYOKSL	442
RESULT 5			
09ZKD7			
ID	09ZKD7	PRELIMINARY;	PRT; 436 AA.
DT	01-MAY-1999	(TEMBLrel. 10, Created)	
DT	01-MAY-1999	(TEMBLrel. 10, Last sequence update)	
DT	01-MAR-2004	(TEMBLrel. 26, Last annotation update)	
DE	ALPHA-(1,3)-FUCOSYLTRANSFERASE.		
GN	OrderedLocustNames=JHPI002;		
OS	Helicobacter pylori J99 (Campylobacter pylori J99).		
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;		
OX	Helicobacteraceae; Helicobacter.		
OX	NCBI_TaxID=85963;		
OX	[1]		
RE	SEQUENCE FROM N.A.		
RX	MEDLINE=99120557; Pubmed=9923682; DOI=10.1038/16495;		
RA	Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown R.D., Doig P.C.,		
RA	Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,		
RA	Tummino P.J., Carnio A., Uita-Nickelsen M., Mills D.M., Ives C.,		
RA	Gibson R., Nerberg D., Mills S.D., Jlang Q., Taylor D.E., Voyis G.F.,		
RA	Trist T.J.;		
RT	Genomic sequence comparison of two unrelated isolates of the human		
RT	gastric pathogen Helicobacter pylori.;		
RL	Nature 397:176-180(1999).		
DR	EMBL; AB001528; AAD06573.1; -.		
DR	PIR; G71862; G71862.		
GO	GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA		
KW	Complete proteome; Glycosyltransferase; Transferase.		
SC	SEQUENCE 436 AA; 50698 MW; 1DB2066A98FA61B CRC64;		

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Query Match Similarity      80.3%; Score 1917; DB 2; Length 436;
Beet Local Similarity      83.1%; Pred. No. 2e-120;
Matches 365; Conservative 20; Mismatches 34; Indels 20; Gaps 4;

Qy      1 MFQPLLDAYVESASIEKXAS--KSPDPKLIAVANWMDGEBIKEFKKSVLTYPFSQRYTA 58
Db      1 MFQPLLDAYFISTPTIKKCTTFSPPEPKLIAVANWVGAE--EPKKSILTYPFLSORYIT 58

Qy      59 LHQNNESSDLVFNSPPLGSAKKILSYONAKKEVFTYGENRVPNPULFDYALGDFDLDFDR 118
Db      59 LHQNNESDVLGSPISGARKILSYONTKRVFTYGENRVPNPULFDYALGDFDLDFDR 118

Qy      119 YLRMPLEYDRLHFKKESVNDFTSPYKLDONSLIYTLKEDSHQKFNHPNLCAVNDSDPL 178
Db      119 YLRMPLEYASLHFKKESVNDFTTAPFKLDONSLIYALKGSHHKFNHPNLCAVNDSDPL 178

Qy      179 KRGVVSFVASNNAEPRNAFYDALNSIEPTVGSSVKNTLGNVYONKSHFSLQYKPNLCE 238
Db      179 KRGFASFVSNFNAFIRNAFYDALNSIEPTVGSSVKNTLGNVYONKSHFSLQYKPNLCE 238

Qy      239 ENSGCGYVTEKILDAYFSHTPIYWGSPVAKDNPKRFPVNVHDFFNNDBAIDVYKYLA 298
Db      239 ENYOGGYVTEKIDAYFSHTPIYWGSPVAKDNPKRFPVNVCDPKNDBAIDVYKYLA 298

Qy      299 THPNAYIDLTYENPNALDGAKEYFDOLSEFKKILAFPKTILENDTIYHKSSTSPMWBCDL 358
Db      299 THPNAYIDLTYENPLNTLDGKAYFYQNLSEFKKILDFPKTILENDTIYH--DNPFIFYRDL 356

Qy      359 DBFLASIDDLRVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL 418
Db      357 NBRFLVAILDLRVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL 402

Qy      419 ELSQNTSPFKIRKAYOKPI 437
Db      403 ELSQNTTFKIRKAYOKSL 421

RESULT 6
ID      068735      PRELIMINARY;      PRT;      432 AA.

```

ALIGNMENTS

RESULT 1

US-10-120-319-1

; Sequence 1, Application US/10120319

; Publication No. US20020164749A1

; GENERAL INFORMATION:

; APPLICANT: Taylor, Diane E.

; APPLICANT: Ge, Zhongming

; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE

; FILE REFERENCE: 07254/049001

; CURRENT APPLICATION NUMBER: US/10/120,319.

; CURRENT FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/048,857

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-06

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 464

; TYPE: PRT

; ORGANISM: Helicobacter pylori

US-10-120-319-1

Query Match 87.4%; Score 2086; DB 13; Length 464;

Best Local Similarity 87.4%; Pred. No. 1.2e-165;

Matches 394; Conservative 15; Mismatches 26; Indels 16; Gaps 2;

QY 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWWGDDEEIKEFKKSVLYFIPFSORYTIALH 60
 |||||
 Db 1 MFQPLLDAYVESASIEKMASKSPPLKIAVANWWGDDEEIKEFKNSVLYFILSORYTTITLH 60
 |||||
 QY 61 QNPNEFSDLVFSNPLGSARKILSYQNAKRVFYTGNEVPNPNLFDYAIGFDELDPRDRYL 120
 |||||
 Db 61 QNPNEFSDLVFGNPLGSARKILSYQNAKRVFYTGNEVPNPNLFDYAIGFDELDPRDRYL 120
 |||||
 QY 121.RMPLYYDRLHHKAESVNDTTPYKLDNSLYTLKKPSHQFKNHPNLCAVNVNDESPLKR 180

Tue May 24 08:36:55 2005

pct-us05-01614

Db 121 RMPYYDRLHHKAESVNDTTAPYKLDNSLYALKKPSHCPEKHPNLCVVNDESDPLKR 180
Qy 181 GVVSVASNANAPMRNAPYDALNSIEPVTGGGSVKNTLGYNVKNKSEFLSQYKPNLCFEN 240
Db 181 GFASFVASNPAPIRNAPYDALNSIEPVTGGGSVRNTLGYNVKNKNEFLSQYKPNLCFEN 240
Qy 241 SQGYGYVTEKILDAYFSHTIPIYWGPSVAKDFNPKFVNVDHFNDFDEAIDYIKYLHTH 300
Db 241 TQGYGYVTEKIIDAYFSHTIPIYWGPSVAKDFNPKSFVNVDHFNDFDEAIDYIKYLHTH 300
Qy 301 PNAYLDMLYENPLNALDGKAYFYQDLSFKKILAPFKTILENDTIYHKSSTSPMWECDLDE 360
Db 301 KNAYLDMLYENPLNTLDGKAYFYQNLSEFKKILAPFKTILENDTIYH--DNPPIFCRDLNE 358
Qy 361 PLASIDDLRV-----NYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV 406
Db 359 PLVTIDDLRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRVNYDDLVRV 418
Qy 407 YERLLQNASPILLELSONTSFKIYRKAYQKPI 437
Db 419 YERLLSKATPILLELSONTTSKIYRKAYQKSL 449

RESULT 2
US-10-189-977-1
; Sequence 1, Application US/10189977
; Publication No. US20030166211A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Scott

ORGANISM: Helicobacter pylori
US-10-189-977-7

Query Match 86.8%; Score 2073; DB 14; Length 478;
Best Local Similarity 84.5%; Pred. No. 1.5e-164;
Matches 393; Conservative 15; Mismatches 27; Indels 30; Gaps 2;

QY 1 MFOPLDAYVESASIERKASKEPPPLKIAVANMMGDEBIKEFKKSVLYIFISQRYTIALH 60
DB 1 MFOPLDAYVESASIERKASKEPPPLKIAVANMMGDEBIKEFKKSVLYIFISQRYTIALH 60
QY 61 QNNEFSDDLVSFNPGLSARKILSYONAKRVFTYGENEVNPNLPDYAIGFDELDFDRYL 120
DB 61 QNNEFSDDLVSFNPGLSARKILSYONAKRVFTYGENEVNPNLPDYAIGFDELDFDRYL 120
QY 121 RMPLYDRLHHRKASVNDTTPPYKDKNSLYTLKKPSHOKENHPNLCAVNDSDPLKR 180
DB 121 RMPLYDRLHHRKASVNDTTPPYKDKNSLYTLKKPSHOKENHPNLCAVNDSDPLKR 180
QY 181 GVSFVASNANAPMNAFPAALNSIEPVYGGSVKNTLGYNVKNSKSEFLSQYKFNLCFEN 240
DB 181 GVSFVASNANAPMNAFPAALNSIEPVYGGSVKNTLGYNVKNSKSEFLSQYKFNLCFEN 240
QY 241 SOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
DB 241 SOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
QY 241 TOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
DB 241 TOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
QY 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
DB 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
QY 301 KNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
DB 301 KNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
QY 361 PLASIDDLRV-----NYDDLRVNYDDLRYNYDDLRYN 392
DB 361 PLASIDDLRV-----NYDDLRVNYDDLRYNYDDLRYN 392
QY 359 PLVTIDDLRVNYDDLRYNYDDLRYNYDDLRYNYDDLRYN 418
DB 359 PLVTIDDLRVNYDDLRYNYDDLRYNYDDLRYNYDDLRYN 418
QY 393 YDDLRYNYDDLRYNYDDLRYNYDDLRYNYDDLRYNYDDLRYN 437
DB 419 YDDLRYNYDDLRYNYDDLRYNYDDLRYNYDDLRYNYDDLRYN 463

RESULT 7

US-09-733-524-1
; Sequence 1, Application US/09733524
; Patent No. US200200683472A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the University of Alberta, a Canada Corporation
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ALPHA-1,3
; TITLE OF INVENTION: FUCOSYLTRANSFERASES AND EXPRESSION SYSTEMS FOR MAKING AND
; TITLE OF INVENTION: EXPRESSING THEM
; FILE REFERENCE: 07254/049002
; CURRENT APPLICATION NUMBER: US/09/733,524
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,857
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Helicobacter pylori fucosyltransferase
US-09-733-524-1

Query Match 86.8%; Score 2073; DB 9; Length 501;
Best Local Similarity 87.1%; Pred. No. 1.6e-164;
Matches 393; Conservative 15; Mismatches 27; Indels 16; Gaps 2;

QY 1 MFOPLDAYVESASIERKASKEPPPLKIAVANMMGDEBIKEFKKSVLYIFISQRYTIALH 60
DB 1 MFOPLDAYVESASIERKASKEPPPLKIAVANMMGDEBIKEFKKSVLYIFISQRYTIALH 60

QY 61 QNNEFSDDLVSFNPGLSARKILSYONAKRVFTYGENEVNPNLPDYAIGFDELDFDRYL 120
DB 61 QNNEFSDDLVSFNPGLSARKILSYONAKRVFTYGENEVNPNLPDYAIGFDELDFDRYL 120
QY 121 RMPLYDRLHHRKASVNDTTPPYKDKNSLYTLKKPSHOKENHPNLCAVNDSDPLKR 180
DB 121 RMPLYDRLHHRKASVNDTTPPYKDKNSLYTLKKPSHOKENHPNLCAVNDSDPLKR 180
QY 181 GVSFVASNANAPMNAFPAALNSIEPVYGGSVKNTLGYNVKNSKSEFLSQYKFNLCFEN 240
DB 181 GVSFVASNANAPMNAFPAALNSIEPVYGGSVKNTLGYNVKNSKSEFLSQYKFNLCFEN 240
QY 241 SOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
DB 241 SOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
QY 241 TOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
DB 241 TOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
QY 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
DB 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
QY 301 KNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
DB 301 KNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
QY 361 PLASIDDLRV-----NYDDLRVNYDDLRYNYDDLRYN 406
DB 361 PLASIDDLRV-----NYDDLRVNYDDLRYNYDDLRYN 406
QY 359 PLVTIDDLRVNYDDLRYNYDDLRYNYDDLRYNYDDLRYN 418
DB 359 PLVTIDDLRVNYDDLRYNYDDLRYNYDDLRYNYDDLRYN 418
QY 407 YERLONASPLLELSONTSFKIYRKAYOKPI 437
DB 419 YERLONASPLLELSONTSFKIYRKAYOKSL 449

RESULT 8

US-10-120-319-8
; Sequence 8, Application US/10120319
; Publication No. US20020164749A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Diane E.
; APPLICANT: Ge, Zhongming
; TITLE OF INVENTION: ALPHA-1, 3-FUCOSYLTRANSFERASE
; FILE REFERENCE: 07254/049001
; CURRENT APPLICATION NUMBER: US/10/120,319
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/092,315
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/048,857
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-120-319-8

Query Match 86.7%; Score 2070.5; DB 13; Length 454;
Best Local Similarity 86.5%; Pred. No. 2.2e-164;
Matches 384; Conservative 27; Mismatches 24; Indels 9; Gaps 2;

QY 1 MFOPLDAYVESASIERKASKEPPPLKIAVANMMGDEBIKEFKKSVLYIFISQRYTIALH 60
DB 1 MFOPLDAYVESASIERKASKEPPPLKIAVANMMGDEBIKEFKKSVLYIFISQRYTIALH 60
QY 61 QNNEFSDDLVSFNPGLSARKILSYONAKRVFTYGENEVNPNLPDYAIGFDELDFDRYL 120
DB 61 QNNEFSDDLVSFNPGLSARKILSYONAKRVFTYGENEVNPNLPDYAIGFDELDFDRYL 120
QY 121 RMPLYDRLHHRKASVNDTTPPYKDKNSLYTLKKPSHOKENHPNLCAVNDSDPLKR 180
DB 121 RMPLYDRLHHRKASVNDTTPPYKDKNSLYTLKKPSHOKENHPNLCAVNDSDPLKR 180
QY 181 GVSFVASNANAPMNAFPAALNSIEPVYGGSVKNTLGYNVKNSKSEFLSQYKFNLCFEN 240
DB 181 GVSFVASNANAPMNAFPAALNSIEPVYGGSVKNTLGYNVKNSKSEFLSQYKFNLCFEN 240
QY 241 SOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
DB 241 SOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
QY 241 TOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
DB 241 TOGYGVTEKILDAYFSHTIPIYWGSPSYAKDPNPKFVNVHDPPNPDALDIYIKYLAHT 300
QY 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
DB 301 PNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
QY 301 KNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
DB 301 KNAYLDMLEPNPLALDGAIFYODLSFKKILAFKFTILENDTIYHKSSTSPMWECDLDE 360
QY 361 PLASIDDLRV-----NYDDLRVNYDDLRYNYDDLRYN 406
DB 361 PLASIDDLRV-----NYDDLRVNYDDLRYNYDDLRYN 406
QY 359 PLVTIDDLRVNYDDLRYNYDDLRYNYDDLRYNYDDLRYN 418
DB 359 PLVTIDDLRVNYDDLRYNYDDLRYNYDDLRYNYDDLRYN 418
QY 407 YERLONASPLLELSONTSFKIYRKAYOKPI 437
DB 419 YERLONASPLLELSONTSFKIYRKAYOKSL 449